

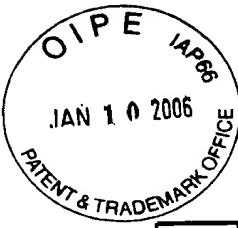


PROTEIN	DESCRIPTION	REFERENCE ¹	mRNA/gene Sequence ²
VOLTAGE-GATED ION CHANNEL	K+ CHANNEL BETA 1A SUBUNIT	Hs.45090	U33428 L39833 L47665
SODIUM CHANNEL	VOLTAGE DEPENDANT SODIUM CHANNEL		
CALCIUM CHANNEL	DIHYDROPYRIDINE-SENSITIVE L-TYPE, CALCIUM CHANNEL BETA-1-B1 SUBUNIT	Hs.635	L0611 M92392 M76560
	DIHYDROPYRIDINE-SENSITIVE L-TYPE CALCIUM CHANNEL ALPHA-1 SUBUNIT (CACNLIA3), NEURONAL DHP-SENSITIVE VOLTAGE-DEPENDENT, CALCIUM CHANNEL ALPHA-2b SUBUNIT	Hs.1294	L33798 U30707
	DIHYDROPYRIDINE-SENSITIVE 1-TYPE SKELETAL MUSCLE CALCIUM CHANNEL GAMMA SUBUNIT	Hs.1296	L07738 Z19603
	NEURONAL DHP-SENSITIVE VOLTAGE-DEPENDENT, CALCIUM CHANNEL ALPHA-1D SUBUNIT	Hs.23838	M76558 M83556 D43747
	PUTATIVE CALCIUM INFLUX CHANNEL (htrp3)	H.24852	U47050 Y13758
	VOLTAGE-DEPENDENT CALCIUM CHANNEL ALPHA-1 E-3	Hs.65441	L29385 L29384 L27745
	N-TYPE CALCIUM CHANNEL ALPHA- SUBUNIT	Hs.69949	M94172 M94173
	VOLTAGE-DEPENDENT L-TYPE Ca CHANNEL ALPHA 1 SUBUNIT	Hs.89925	L29536 L29534 M92269

1 GENBANK REFERENCE DESIGNATION FOR PROTEIN. PROTEINS WITH NO DESIGNATION ARE REFERENCED IN THIS TEXT.

2 GENBANK mRNA OR GENE SEQUENCE REFERENCE DESIGNATION.

FIG. 1-A



2/27

PROTEIN	DESCRIPTION	REFERENCE	mRNA/gene Sequence
LIGAND-GATED CHANNEL	GAMMA-AMINO BUTYRIC ACID (GABA) RECEPTOR NICOTINIC ACETYLCHOLINE RECEPTOR	Hs.16362	AF007891 U52464
G-COUPLED RECEPTOR	P2Y6 RECEPTOR	Hs.784	L08177
	CHEMOKINE (C-C) RECEPTOR 7	Hs.1544	U14910
	HUMAN RPE-RETINAL G PROTEIN-COUPLED RECEPTOR	Hs.11173	U52153 D87327 U24660
	INWARDLY RECTIFYING POTASSIUM CHANNEL KIR3.2		
	G PROTEIN-COUPLED RECEPTOR KINASE GRK4	Hs.32859	L03718 U33054
	G PROTEIN-COUPLED INWARDLY RECTIFYING POTASSIUM CHANNEL Kir3.4	Hs.37168	U52154
	G PROTEIN-ACTIVATED INWARDLY RECTIFYING POTASSIUM CHANNEL HGIRK1/Kir3.1	Hs.37169	U50964
RECEPTOR-GATED CHANNEL	FC FRAGMENT OF IgE HIGH AFFINITY 1, RECEPTOR FOR: BETA POLYPEPTIDE	Hs.30	M89796
	INTERLEUKIN 2 RECEPTOR GAMMA CHAIN	Hs.84	L19546
	CHOLECYSTOKININ A RECEPTOR	Hs.129	L13605 L19315
	PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR	Hs.202	M36035
	CHOLECYSTOKININ B RECEPTOR	Hs.203	L07746 L10822
	GLUCAGON RECEPTOR	Hs.208	L20316
	SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4 PRECURSOR	Hs.220	L11695
	FORMYL PEPTIDE RECEPTOR-LIKE 1	Hs.251	M84562 M88107
	ADENOSINE RECEPTOR A3	Hs.258	L20463 L22607

FIG. 1-B



3/27

PROTEIN	DESCRIPTION	REFERENCE	mRNA/gene Sequence
GROWTH FACTOR RECEPTOR	PLEIOTROPHIN (HEPARIN BINDING GROWTH FACTOR 8, NEURITE GROWTH-PROMOTING FACTOR 1)	Hs.44	M57399
	HEPATOCYTE GROWTH FACTOR ACTIVATOR RECURSOR	Hs.104	D14012
	FIBROBLAST GROWTH FACTOR 9 (GLIA-ACTIVATING FACTOR)	Hs.111	D14838
	INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2	Hs.162	M35410
KINASE	HUMAN GROWTH FACTOR RECEPTOR TYROSINE KINASE (STK-1)	Hs.385	U02687
	PROTO-ONCOGENE C-COT (PROTEIN-SERINE/THREONINE KINASE)	Hs.248	D14497
	RECEPTOR PROTEIN-TYROSINE KINASE SKY	Hs.301	U18934
	CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE IV	Hs.348	D30742 L24959
	CREATINE KINASE B	Hs.669	M16451 L47647
TRANSFERASE	V-raf MURINE SARCOMA VIRAL ONCOGENE HOMOLOG B1	Hs.662	M95712
	GLUCOSAMINYL (N-acetyl) TRANSFERASE 1, CORE 2	Hs.781	M97347 L41415
	GLUTATHIONE S-TRANSFERASE, MICROSMAL	Hs.790	J03746
	UDP GLUCOSYLTRANSFERASE 8 (UDP-GALACTOSE CERAMIDE GALACTOSYLTRANSFERASE)	Hs.57700	U30930 U62899
ISOMERASE	PEPTIDYLPROLYL ISOMERASE B (CYCLOPHILIN B)	Hs.699	
	3-BETA HYDROXY-5-ENE STEROID DEHYDROGENASE TYPE II	Hs.825	M67466 N77144
	GLUCOSE PHOSPHATE ISOMERASE	Hs.944	K03515
PROTEASE	HYDROXY-DELTA-5-STEROID DEHYDROGENASE, 3-BETA- AND STEROID DELTA-ISOMERASE 1	Hs.38586	M27137 M38180
	26S PROTEASE REGULATORY SUBUNIT 4	Hs.548	L02426
	HEPSIN	Hs.823	M18930
	GRANZYME B PRECURSOR	Hs.1051	M17016
DEHYDROGENASE	GLYCINE CLEAVAGE SYSTEM PROTEIN P (GLYCINE DECARBOXYLASE)	Hs.27	M64590
	17 BETA HYDROXYSTEROID DEHYDROGENASE, TYPE 2	Hs.181	L11708

FIG. 1-C



4/27

PROTEIN	DESCRIPTION	REFERENCE	mRNA/gene Sequence
DEHYDROGENASE	XANTHINE DEHYDROGENASE	Hs.250	D11456
	ALCOHOL DEHYDROGENASE 7 SIGMA SUBUNIT (CLASS IV)	Hs.389	U09623 U07821
	SUCCINATE DEHYDROGENASE 2, FLAVOPROTEIN (Fp) SUBUNIT	Hs.469	D30648 L21936
SYTHETASE	LONG CHAIN FATTY ACID ACYL-COA LIGASE FOLYLGLUTAMATE SYNTHETASE	Hs.34	L09229
	GLUTAMATE-CYSTEINE LIGASE (GAMMA-GLUTAMYL CYSTEINE SYNTHETASE), CATALYTIC	Hs.754	M98045
	HYDROXYMETHYLBILANE SYNTHASE	Hs.1673	M90656
DEAMINASE	Dipeptidylpeptidase IV (CD26, ADENOSINE DEAMINASE COMPLEXING PROTEIN 2)	Hs.82609	M95623
	Deoxycytidylate deaminase	Hs.44926	M80536
	AMP deaminase 2	Hs.76894	L12136
ONCOGENE	Adenosine monophosphate deaminase (isoform E) V- <i>rk</i> avian sarcoma virus CT10 oncogene homolog	Hs.82927	U16270
	Thyroid hormone receptor, alpha (avian erythroblastic leukemia viral (v-erb-a) oncogene homolog)	Hs.83918	M84721
	Friend leukemia virus integration I	Hs.16	D10656
	Rap1A, member of RAS oncogene family	Hs.724	M24899
	Thrombopoietin (myeloproliferative leukemia virus oncogene ligand, megakaryocyte growth and development factor)	Hs.736	M98833
	Fibroblast growth factor 4 (heparin secretory transforming protein 1, Kaposi's sarcoma oncogene)	Hs.865	M22995
FOS	V-erb-a avian erythroblastotic leukemia viral oncogene homolog-like 4	Hs.1166	L36051
JUN	P55-c-fos proto-oncogene protein	Hs.1755	J029986 M17446
	C-jun proto-oncogene (JUN)		L07868
	Jun B proto-oncogene		V01512 J04111 M29039

FIG. 1-D



FIG. 1-E



CANINE LV MYOCYTES INFECTED
WITH dGFP or AdHERG

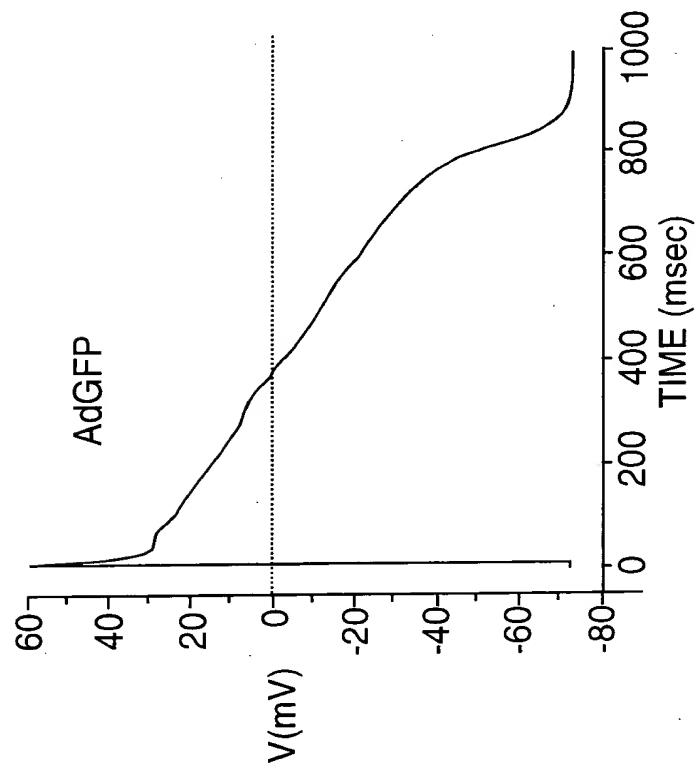


FIG. 2A

CANINE LV MYOCYTES INFECTED
WITH dGFP or AdHERG

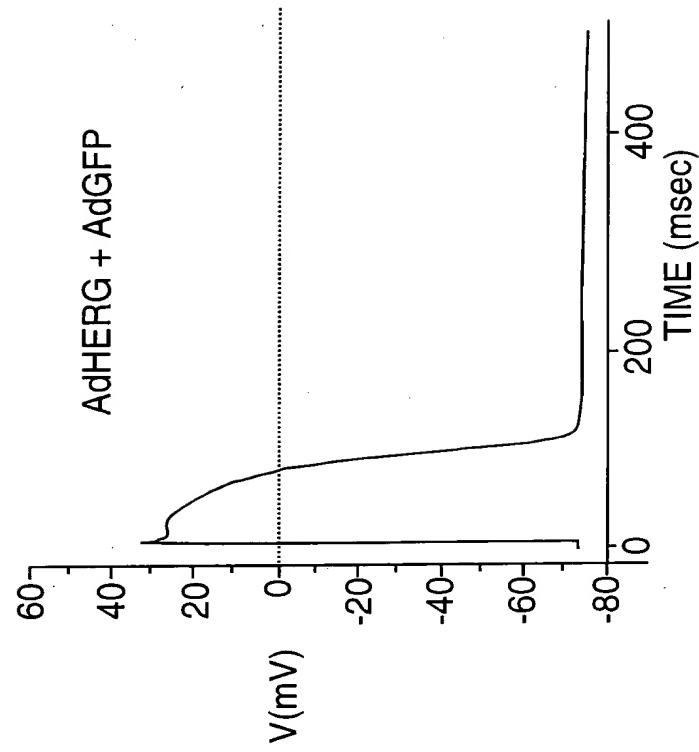


FIG. 2B

6/27



7/27

CANINE LV MYOCYTES INFECTED
WITH dGFP or AdHERG

AdHERG + AdGFP

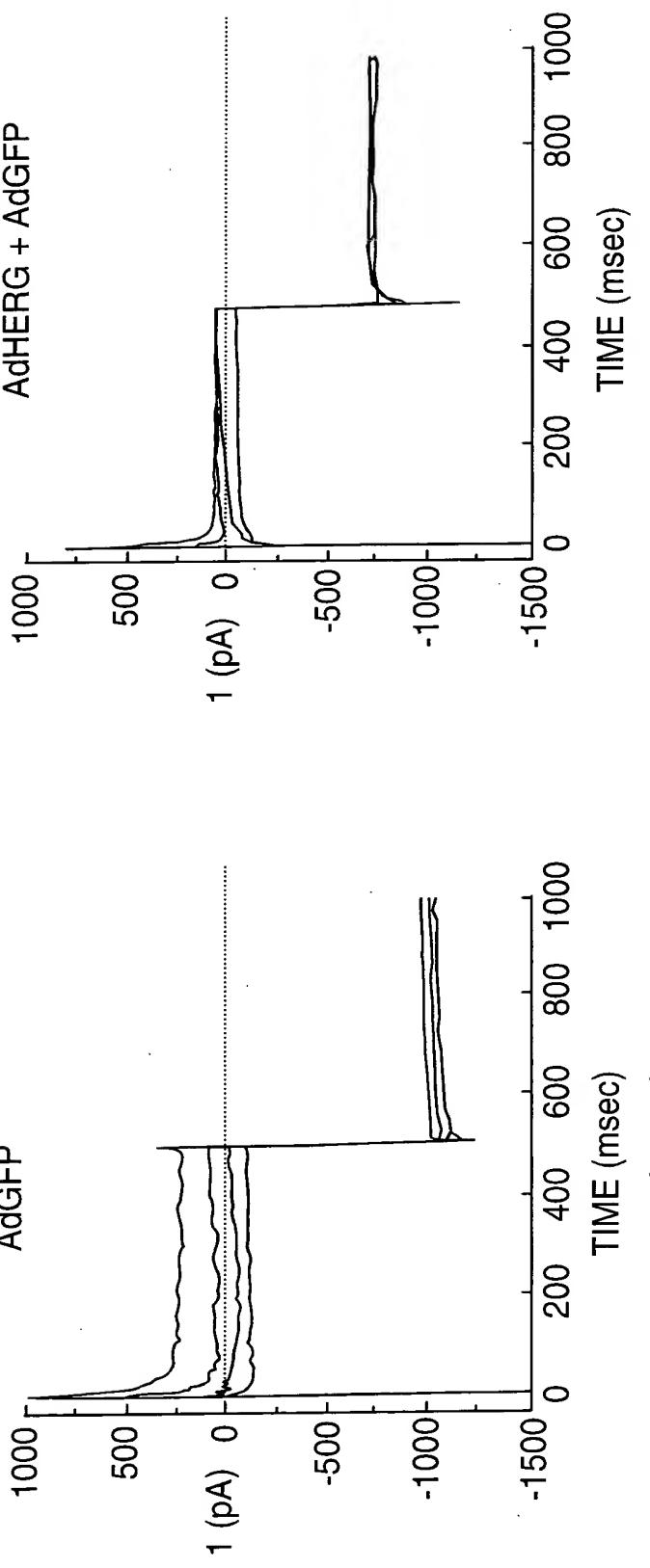


FIG. 2C

FIG. 2D



CANINE LV MYOCYTES INFECTED
WITH dGFP or AdHERG

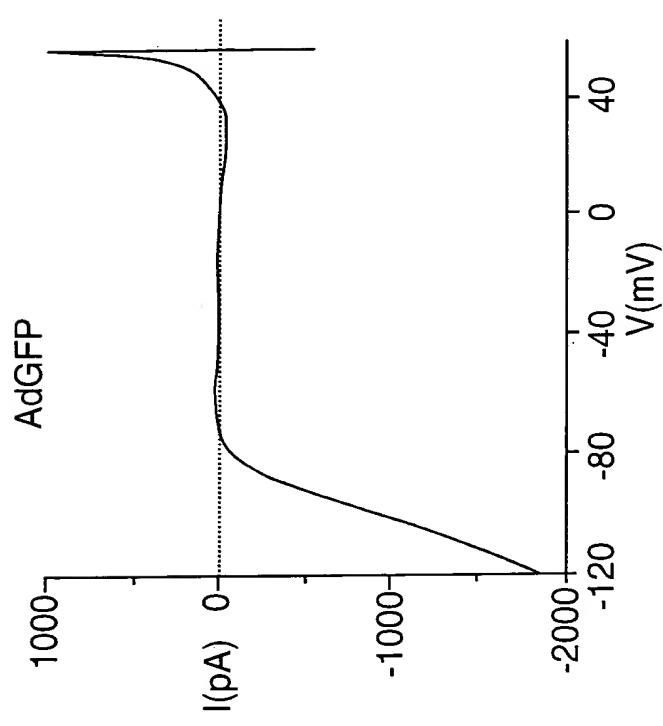


FIG. 2E

CANINE LV MYOCYTES INFECTED
WITH dGFP or AdHERG

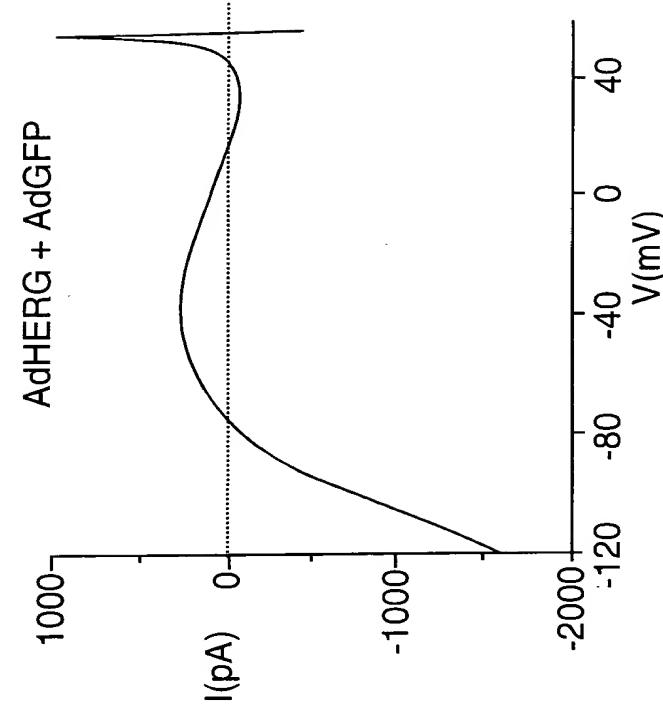


FIG. 2F

8/27



9/27

SCHEMATIC

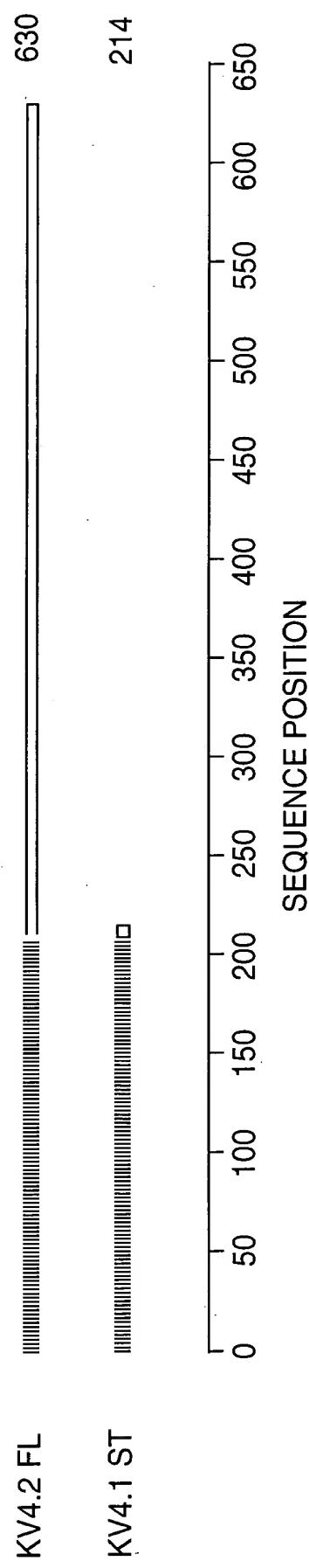


FIG. 3A



ALIGNMENT

KV4.2 FL KV4.2 ST	MAAGVAAWLPFARAAAIGWMPVASGMPAPPROERKRTQDALIVLNVS GTRFQTWQDTLE MAAGVAAWLPFARAAAIGWMPVASGMPAPPROERKRTQDALIVLNVS GTRFQTWQDTLE	60 60
KV4.2 FL KV4.2 ST	RYPDTLLGSSSERDFYHPETQQYFFDRDPDIFTRHILNFYRTGKLHYPRHECISAYDEELA RYPDTLLGSSSERDFYHPETQQYFFDRDPDIFTRHILNFYRTGKLHYPRHECISAYDEELA	120 120
KV4.2 FL KV4.2 ST	FFGLIPEIIIGDCCYEYKDRENAERLQDDADTDNTGESALPTMTARQRVWRAFENPHT FFGLIPEIIIGDCCYEYKDRENAERLQDDADTDNTGESALPTMTARQRVWRAFENPHT	180 180
KV4.2 FL KV4.2 ST	STMALVYYVTGFFIAVSVIANVVE T pcgsspgihikelpcgerayavaffcldtacvmif STMALVYYVTGFFIAVSVIANVVE T gsrhdkih-----	240 214
KV4.2 FL KV4.2 ST	tveyllrlaaapsryrfvrsvmsiidvvailppyyig1vmtdnedvsgafvt1rvfrvfri -----	300 214
KV4.2 FL KV4.2 ST	fkkfsrhsggirlygtlkscaselgfllfsltmaiifatvmyaekgssaskftsipaa -----	360 214
KV4.2 FL KV4.2 ST	fwytivtmttlygdavpktaqkifgsicslsgv1vialpvivnsriyhqngrad -----	420 214
KV4.2 FL KV4.2 ST	krraqkkarlariraaksgsanaymqskrngllsnqlqssedepafvsksgssfetqhkh -----	480 214
KV4.2 FL KV4.2 ST	11hclekttnhefvdeqvfeescmvatvnrpsshsps1sqqgvtsccsrrhkktfri -----	540 214

FIG. 3B



11/27

600
214

pnanvsgshrgsvqelstiqircvertplnsrsslnakmeecvklnceqpyvttaisi

630
214

ptppvttpegddrpespeyssgnivrsal

KV4.2 FL
KV4.2 ST

KV4.2 FL
KV4.2 ST

FIG. 3C



12/27

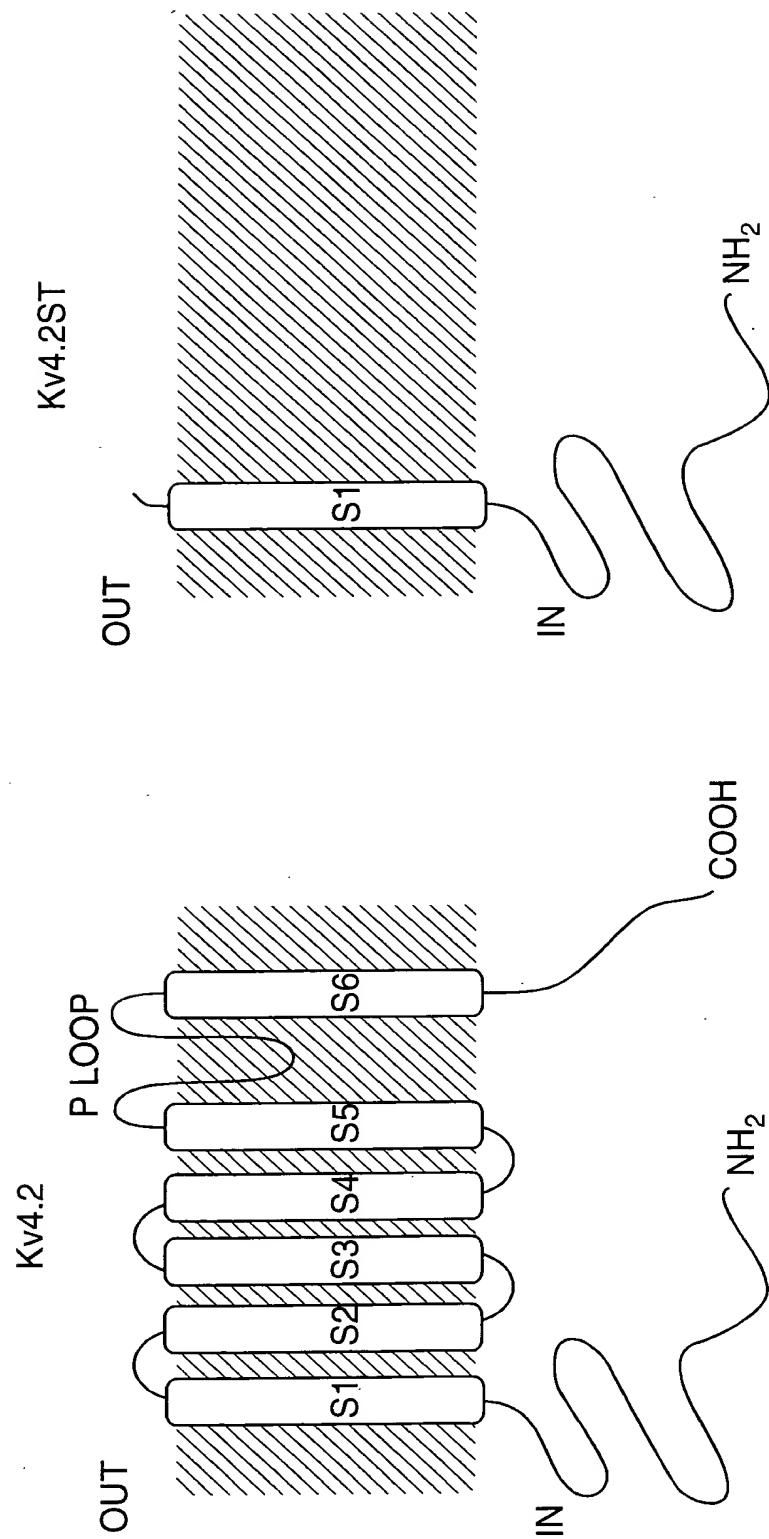


FIG. 4B

FIG. 4A



13/27

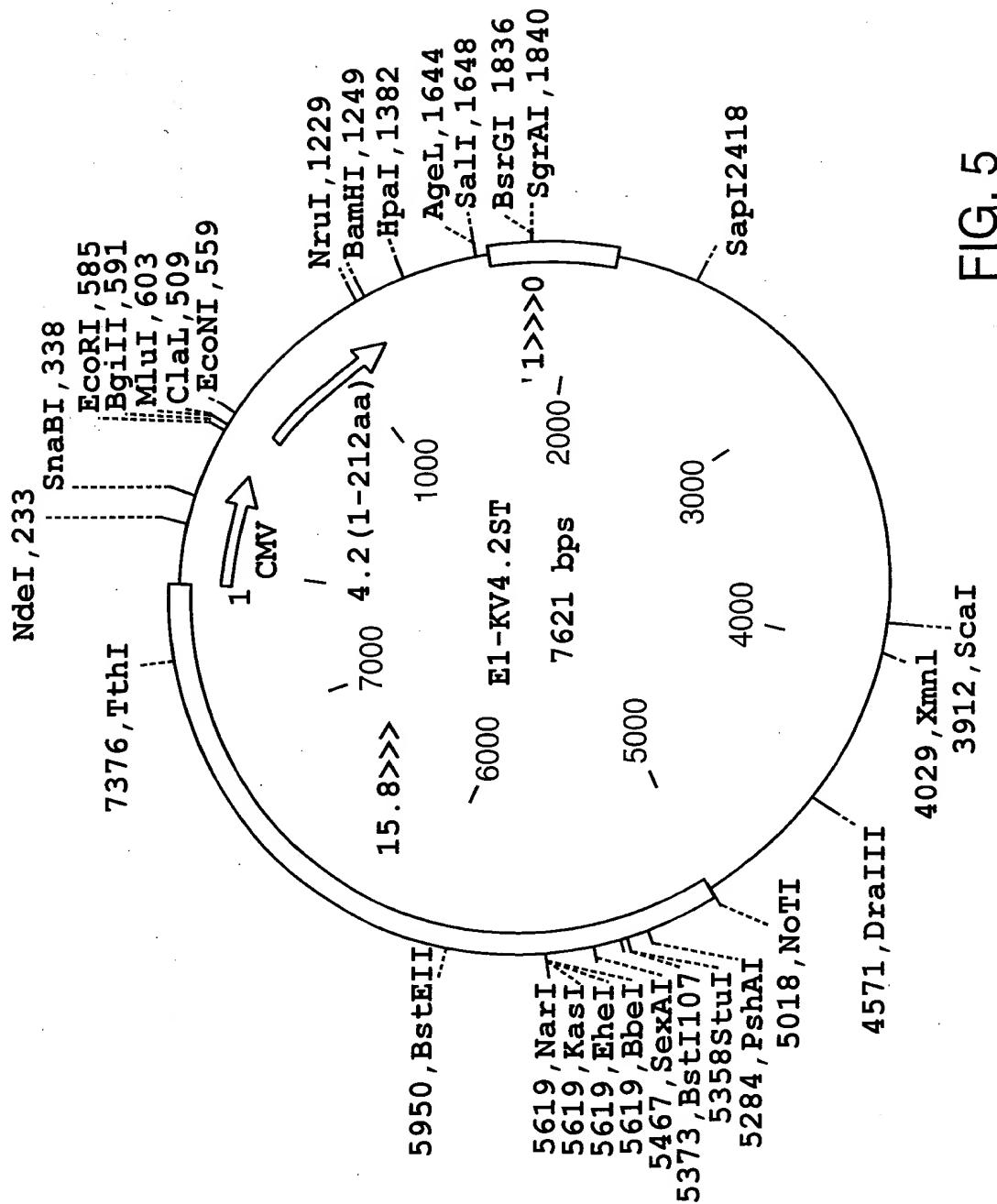


FIG. 5



14/27

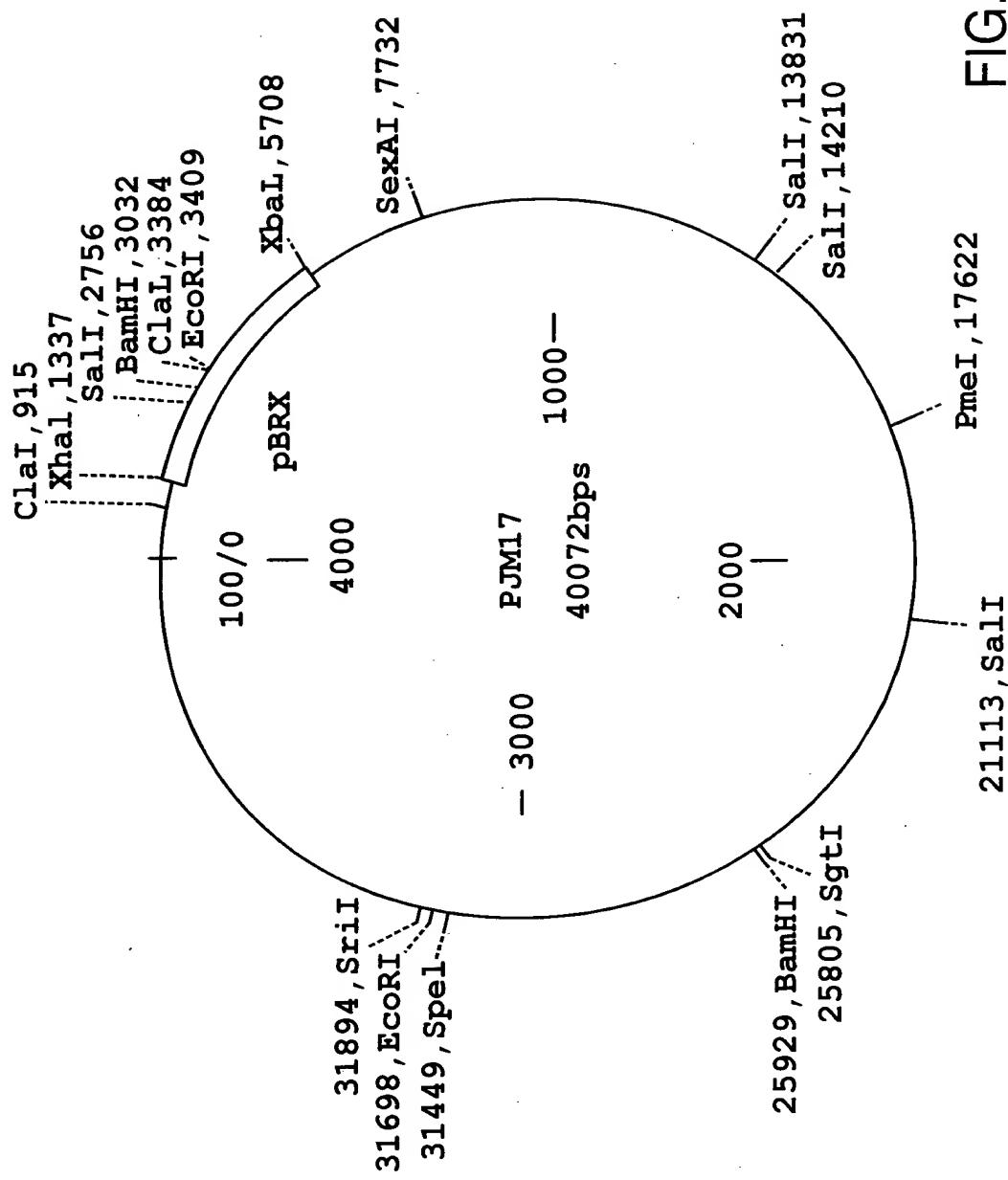
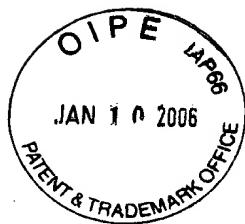
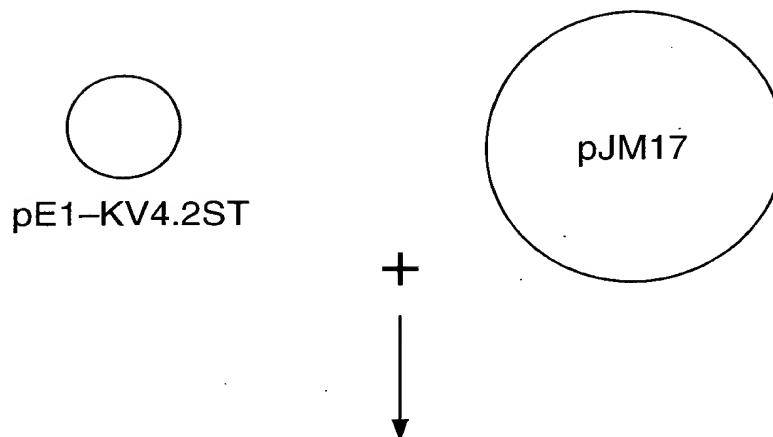


FIG. 6



15/27



AdKv4.2ST

FIG. 7A

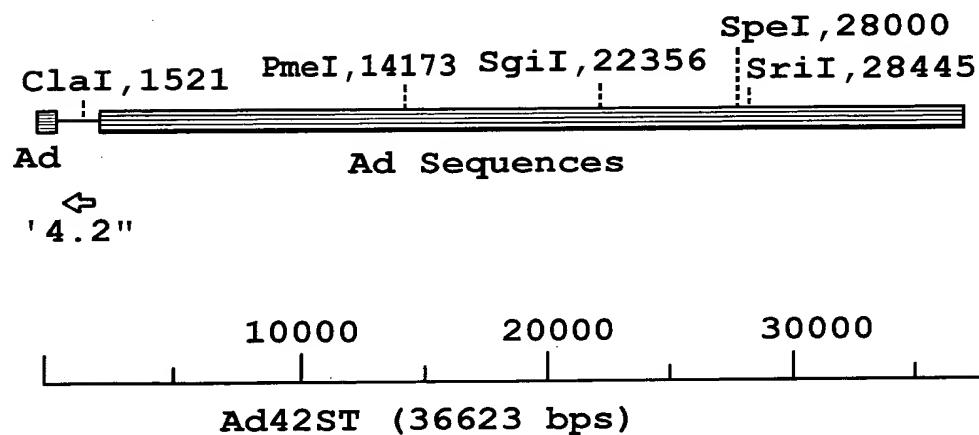


Fig.7B



16/27

1 2 3 4 5 6 7 8 9 10

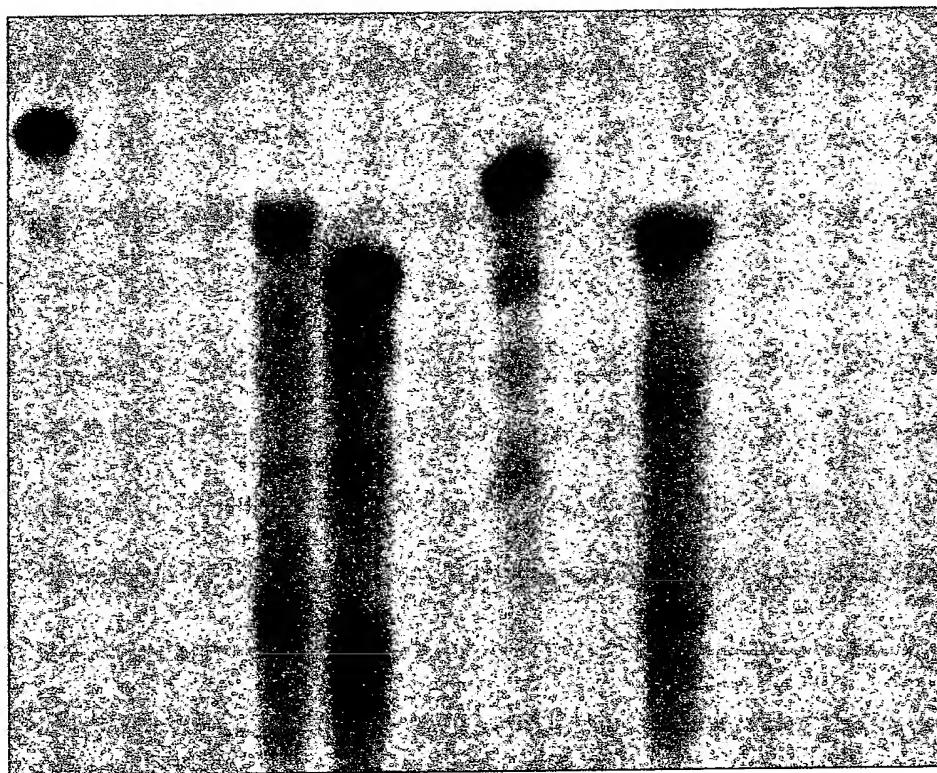
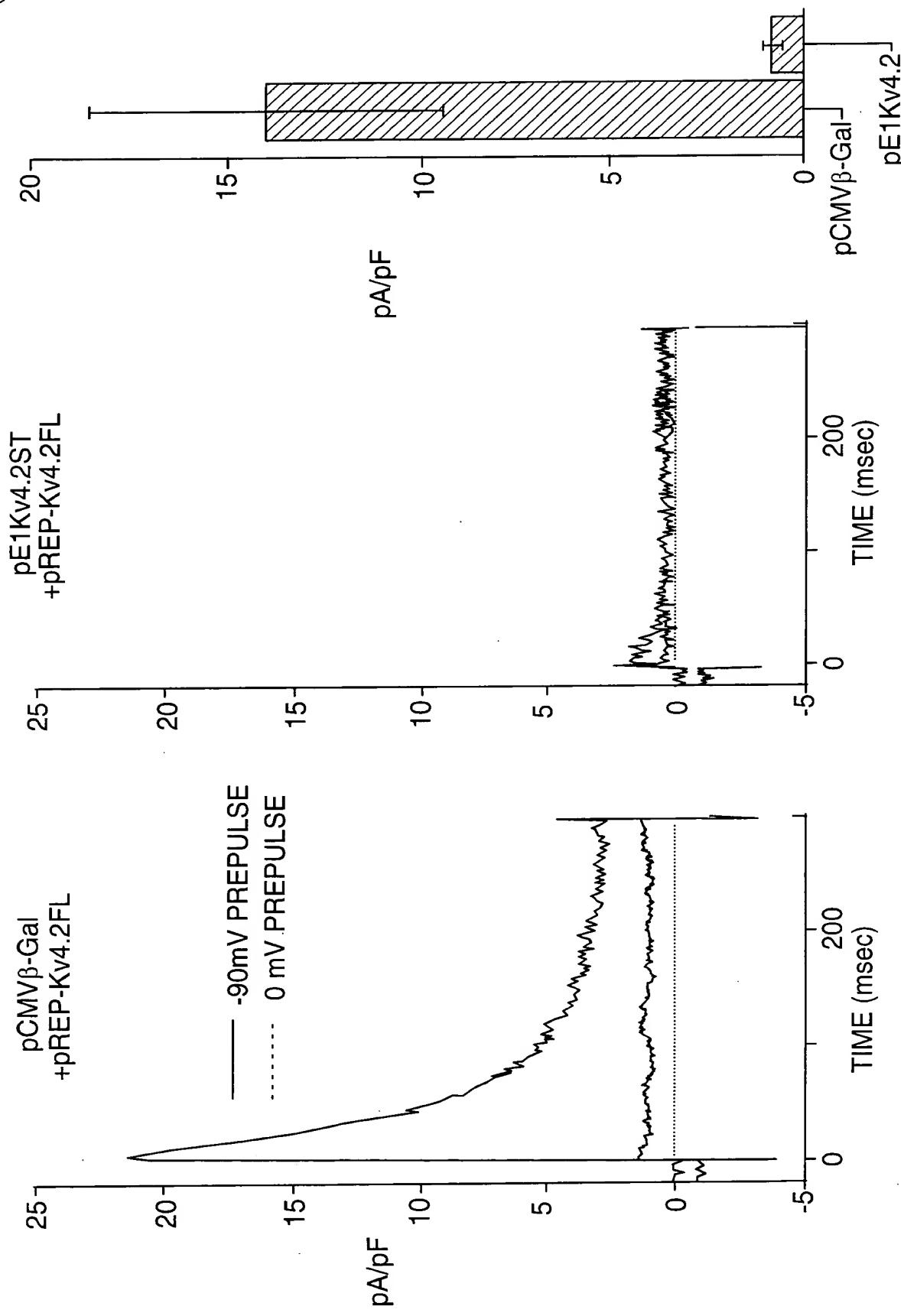


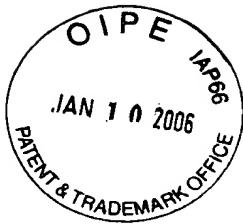
FIG. 8

BEST AVAILABLE COPY



17/27





18/27

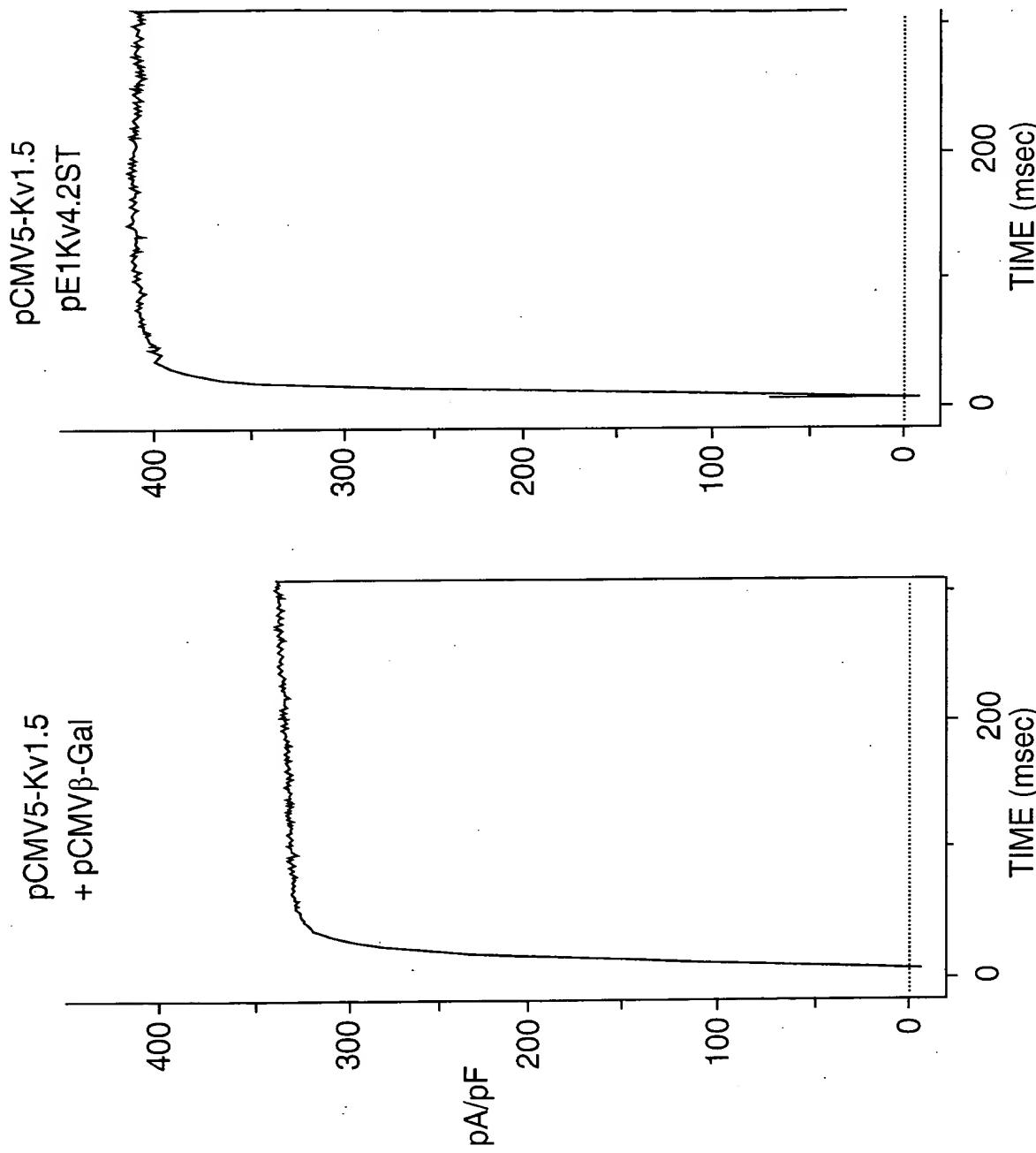


FIG. 9D

FIG. 9E

FIG. 9F



19/27

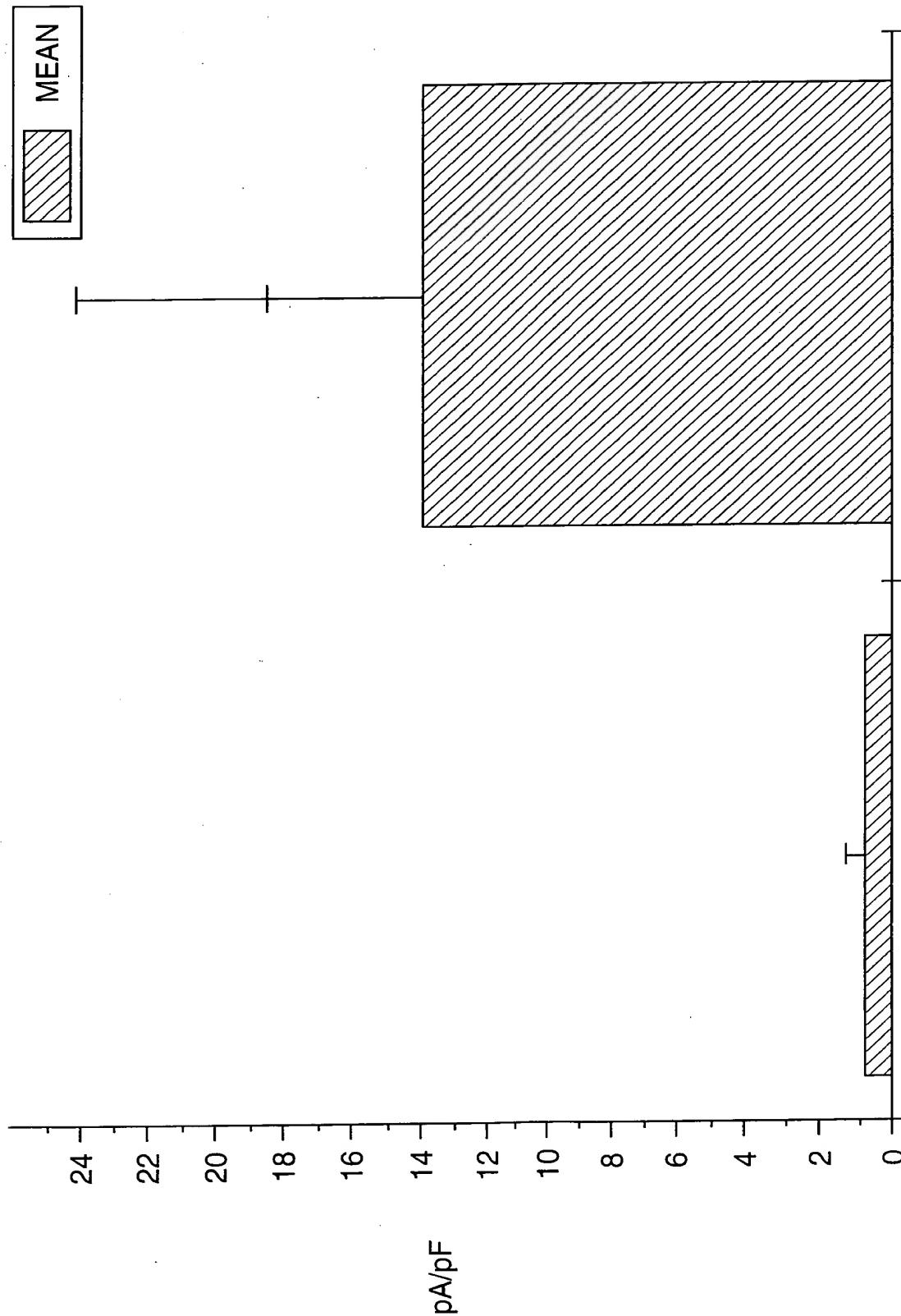


FIG. 10B

FIG. 10A



20/27

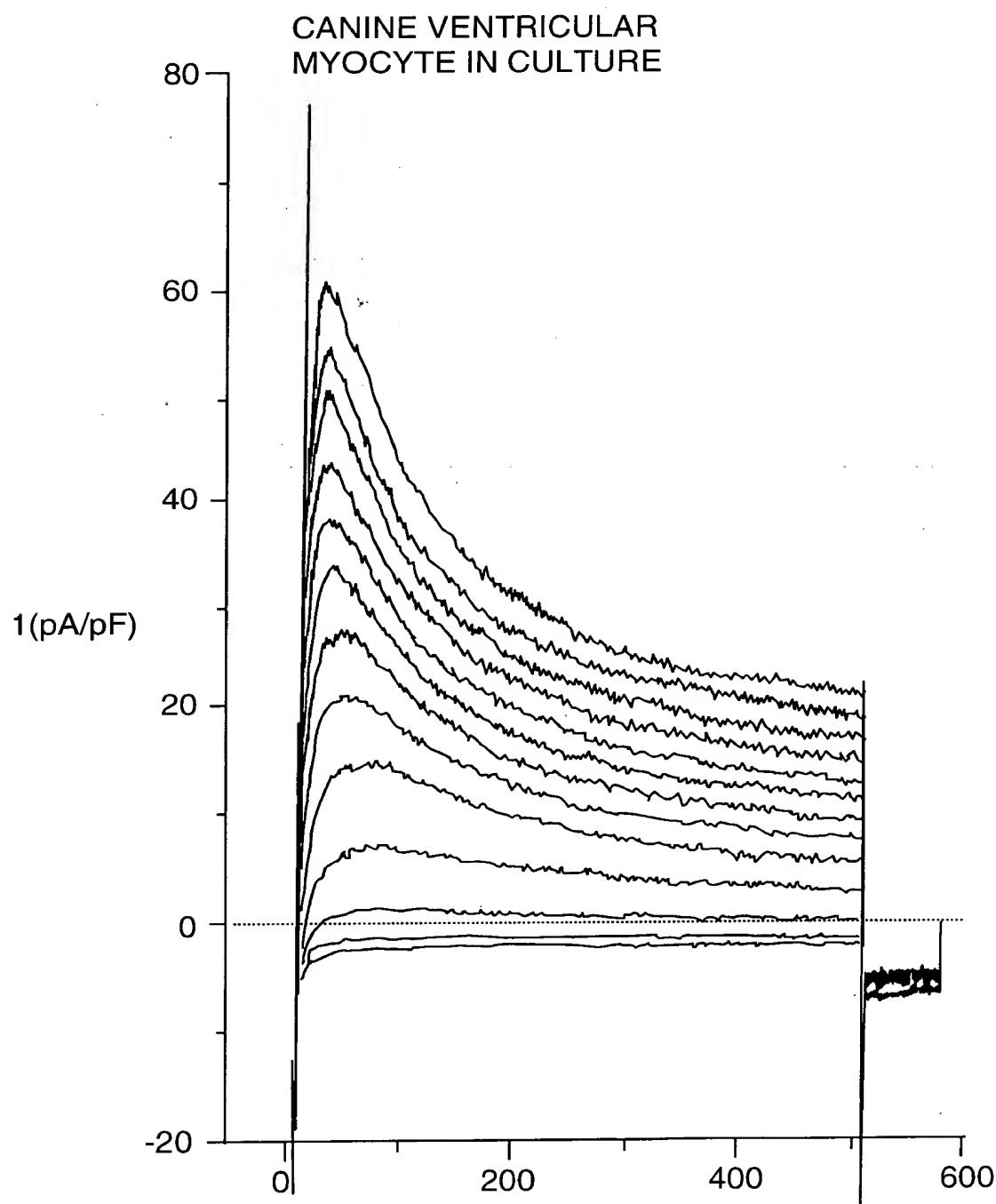


FIG. 11A



21/27

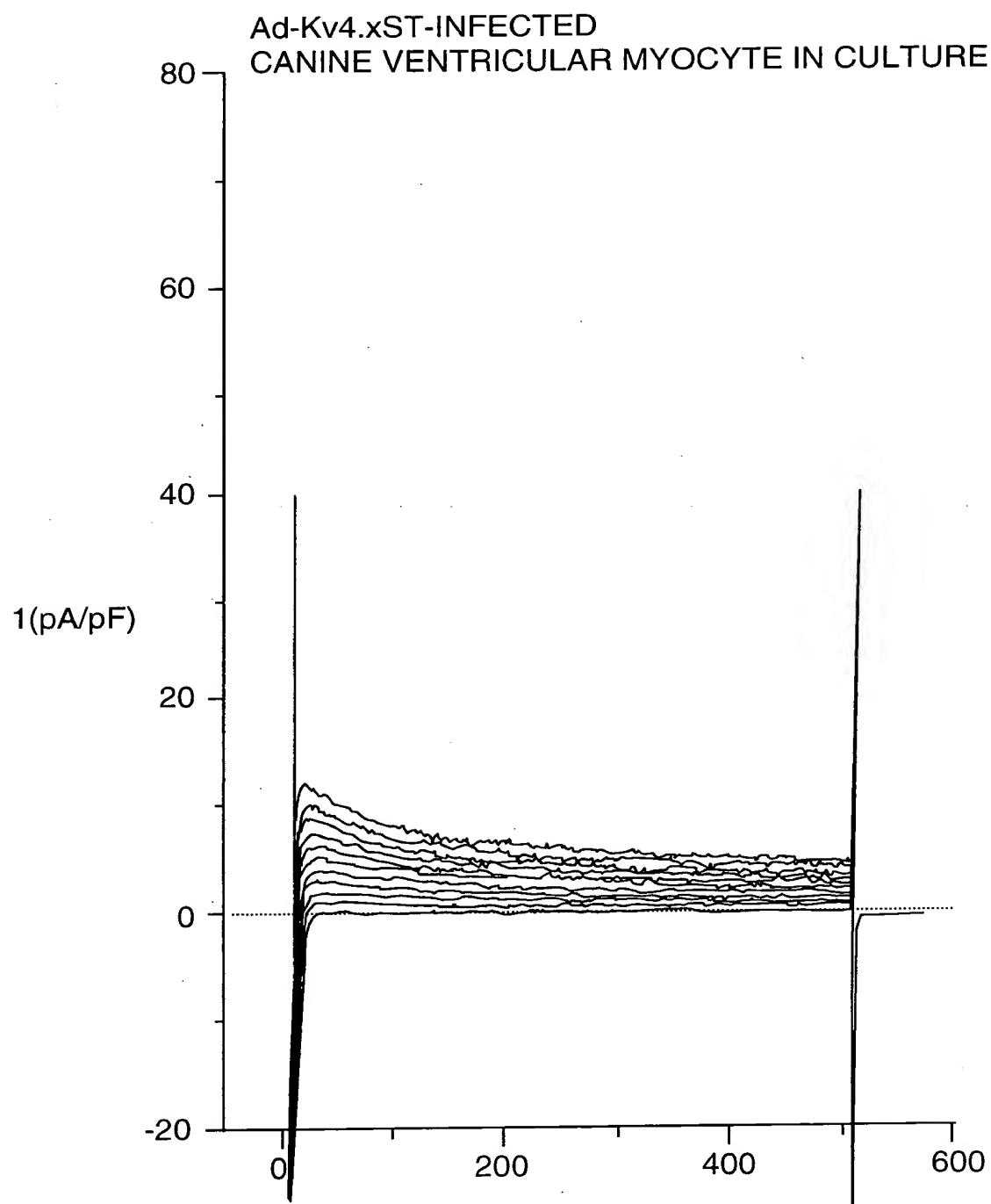


FIG. 11B

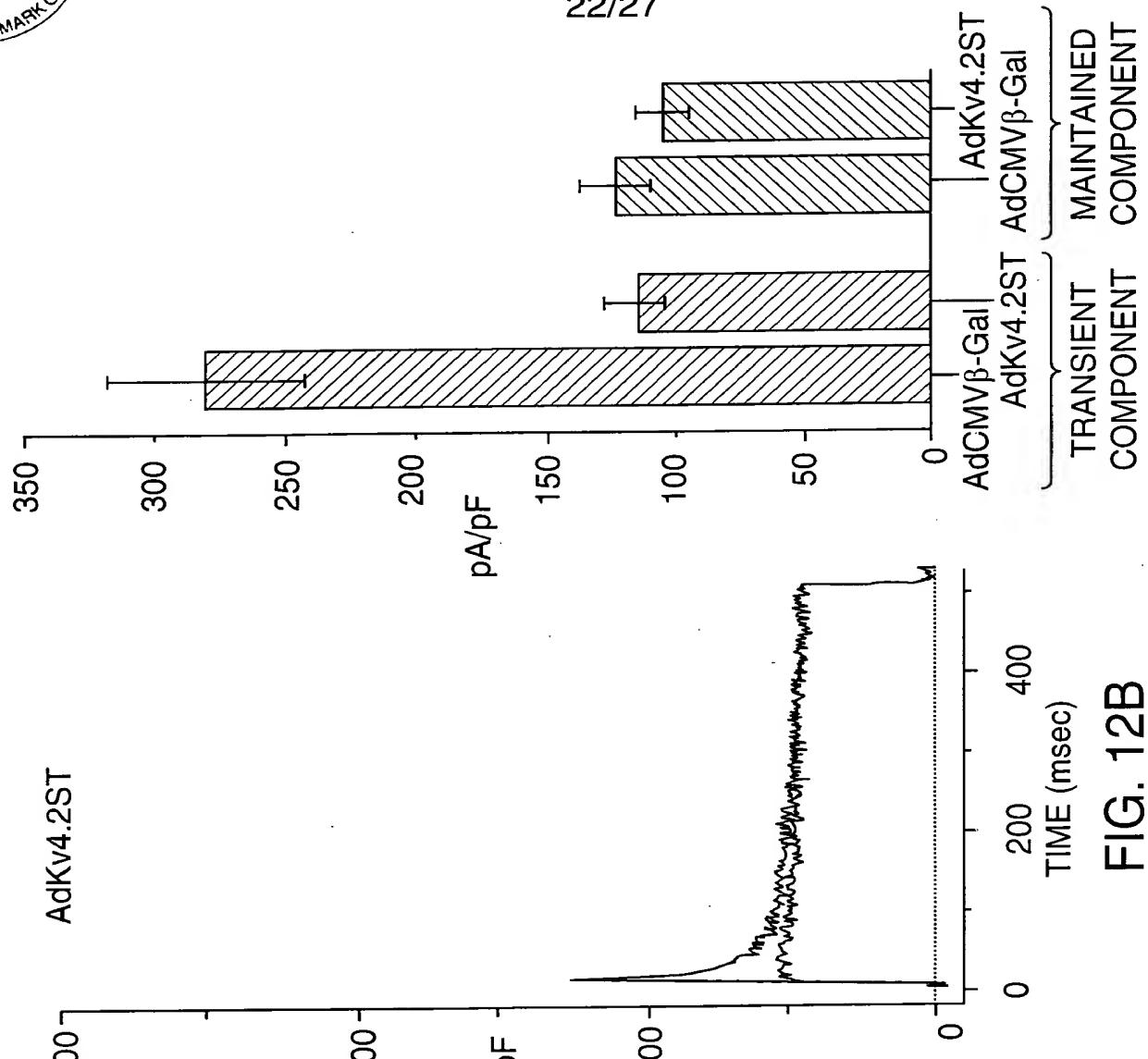
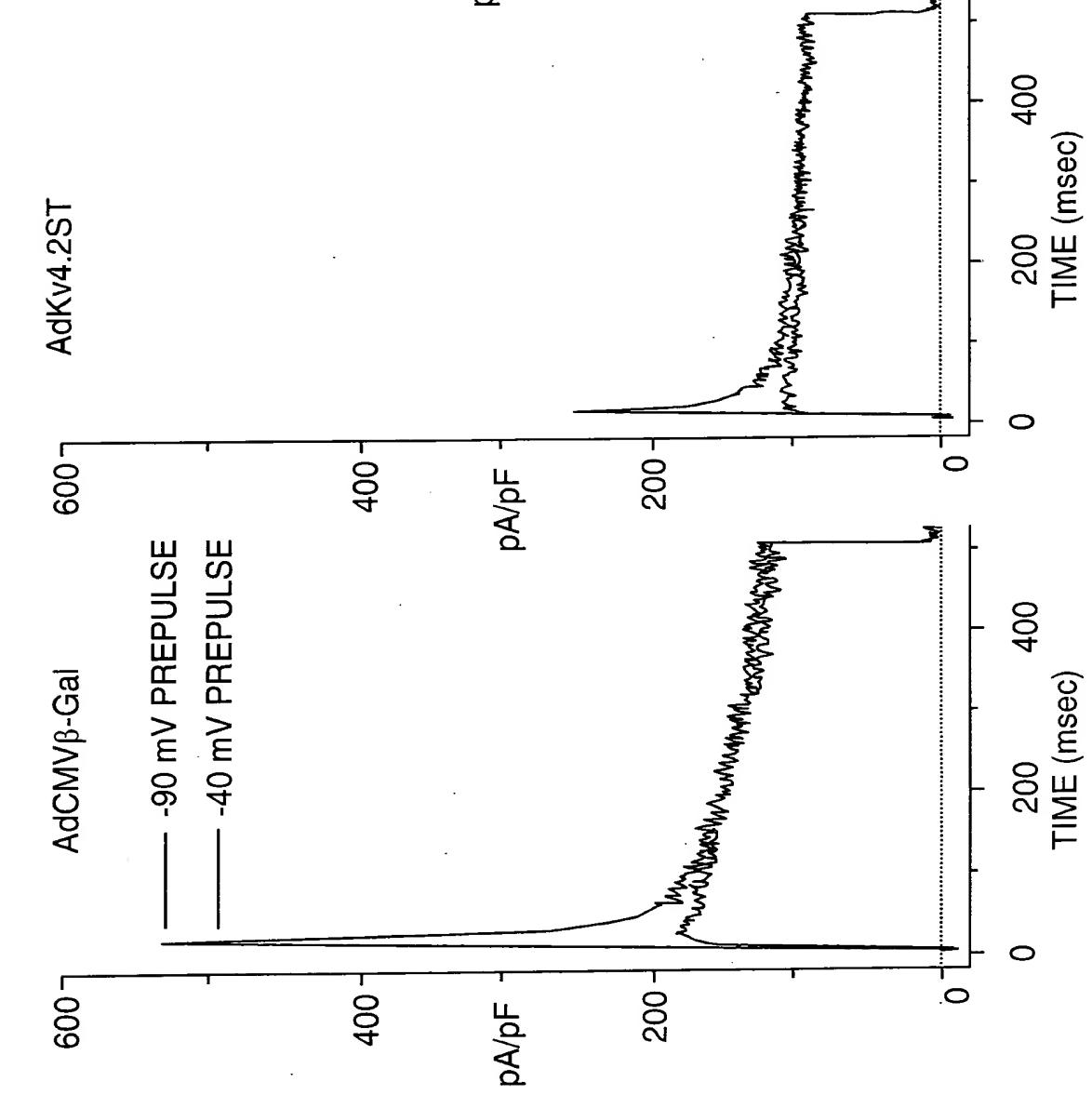


FIG. 12C



23/27

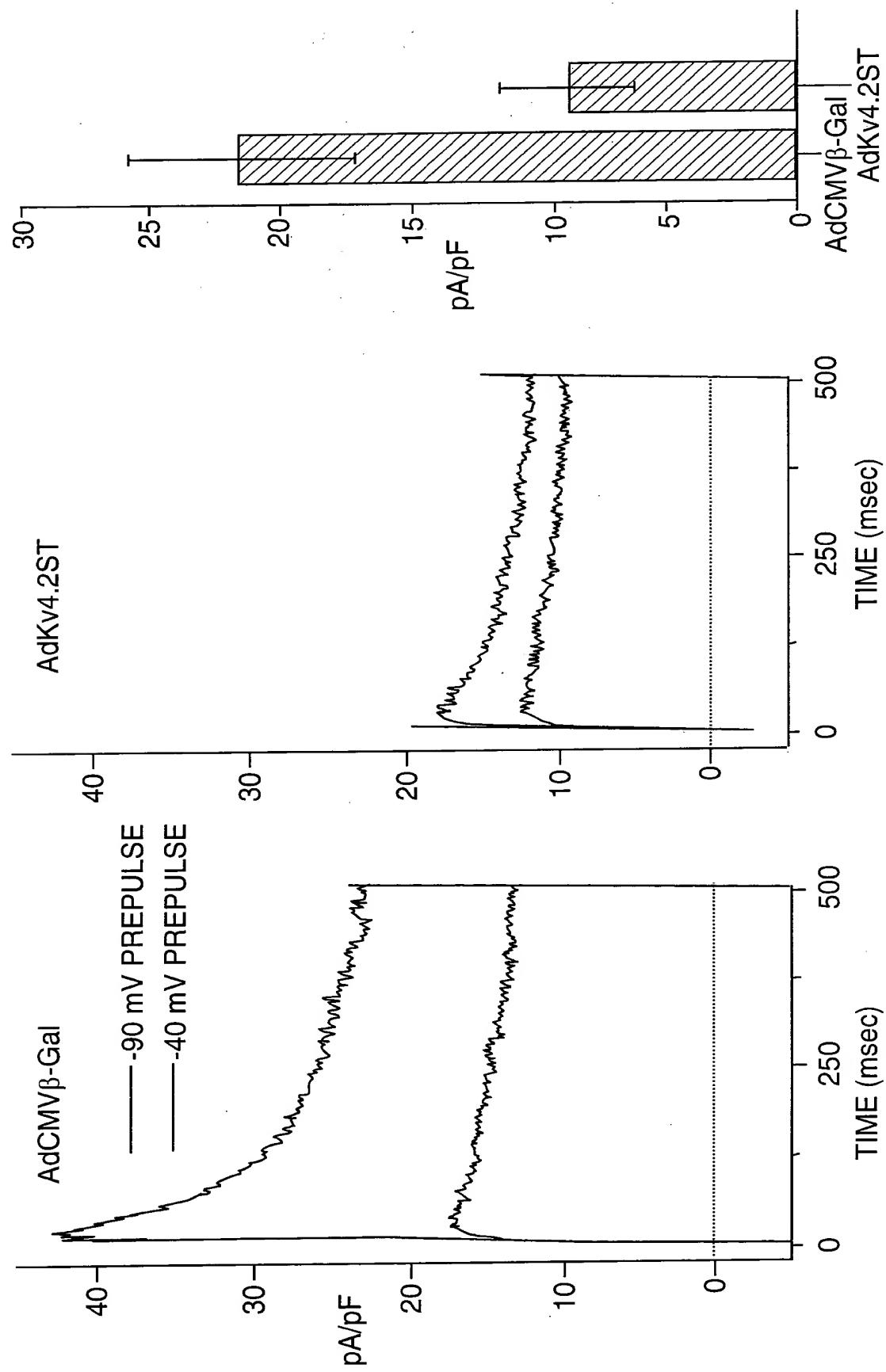


FIG. 13A

FIG. 13B

FIG. 13C



24/27

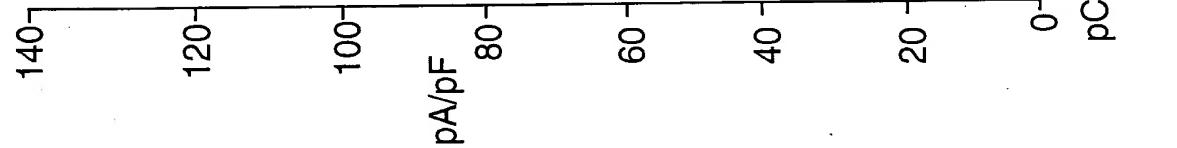
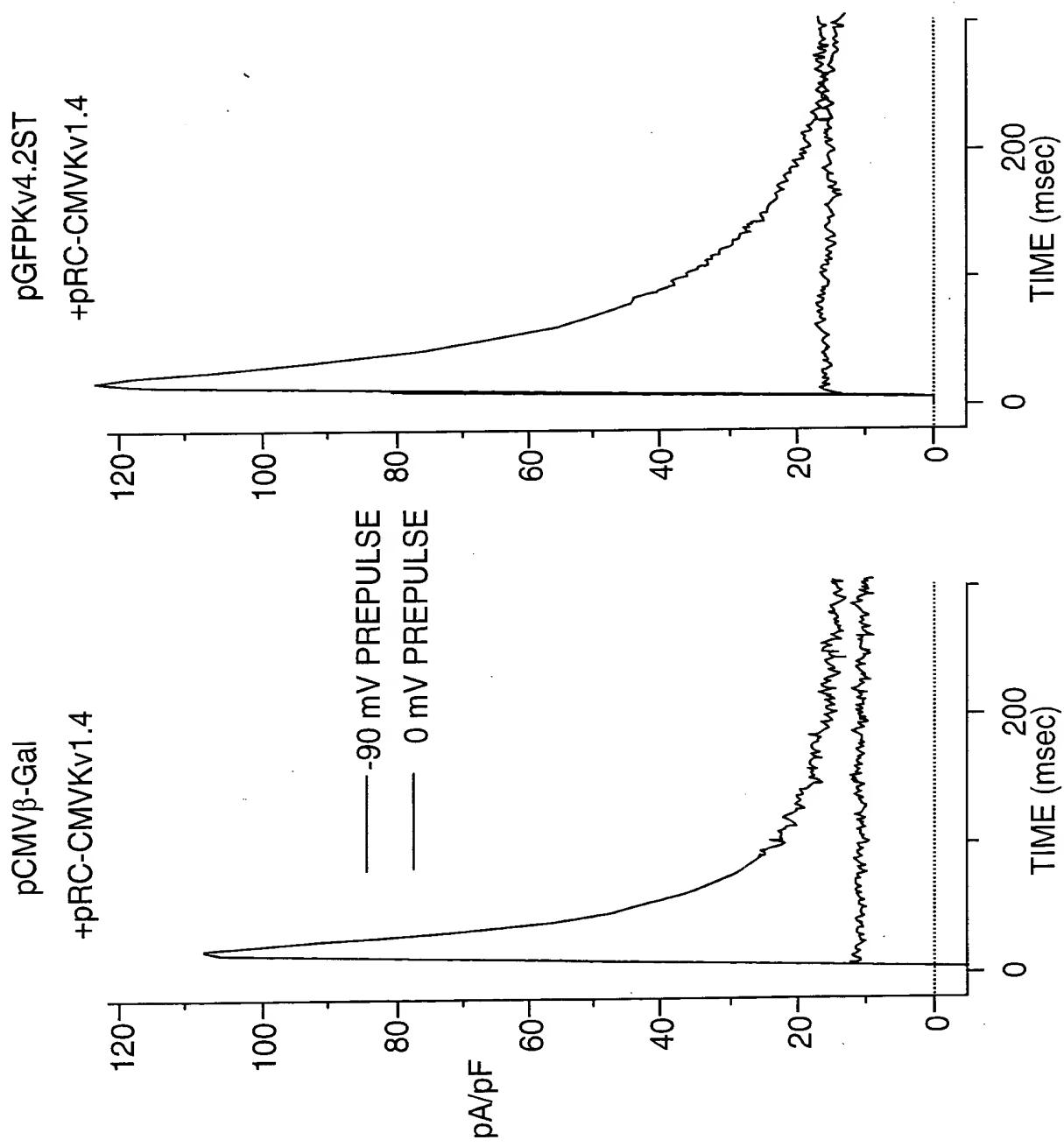


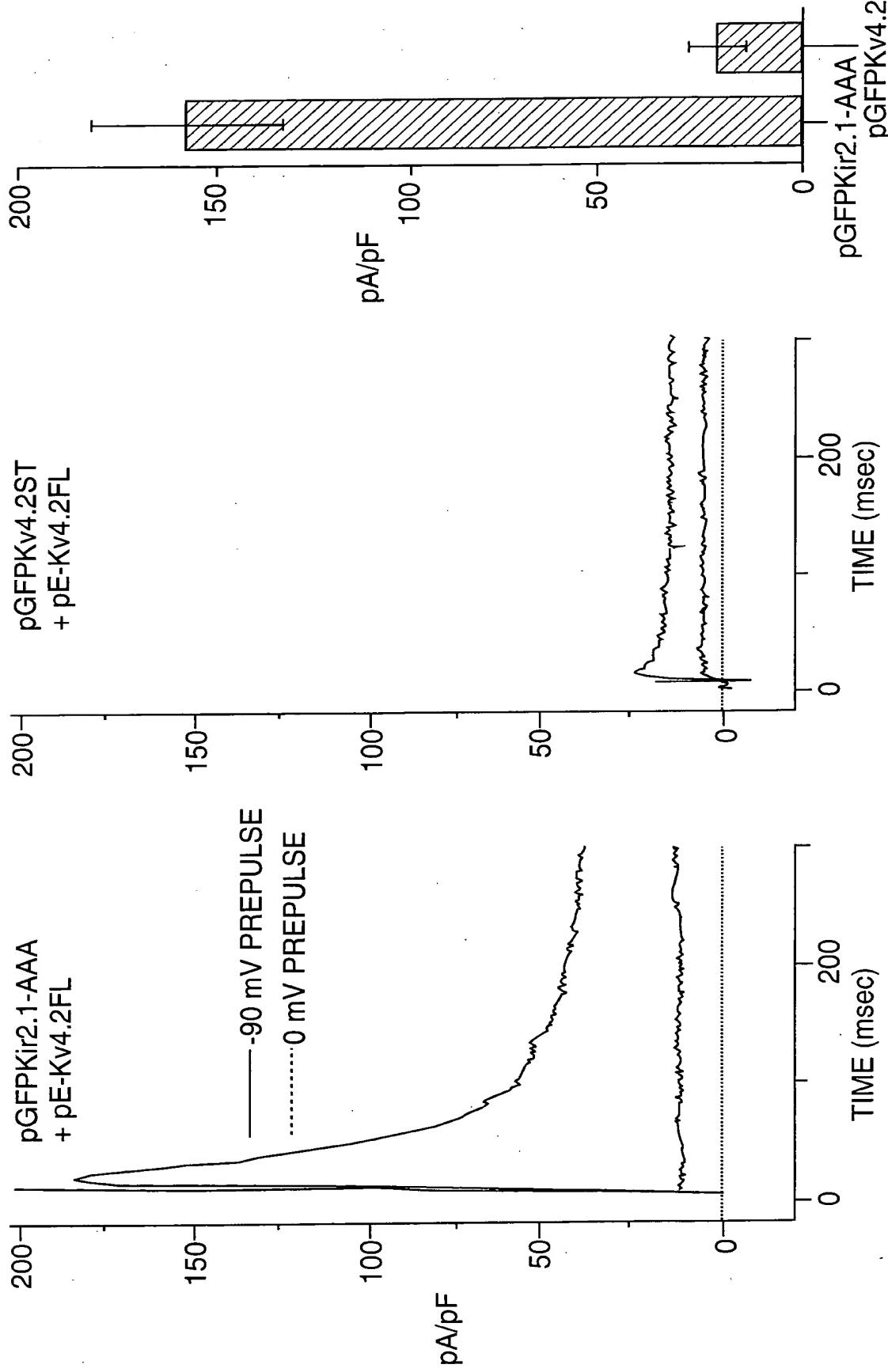
FIG. 14C

FIG. 14B

FIG. 14A



25/27





26/27

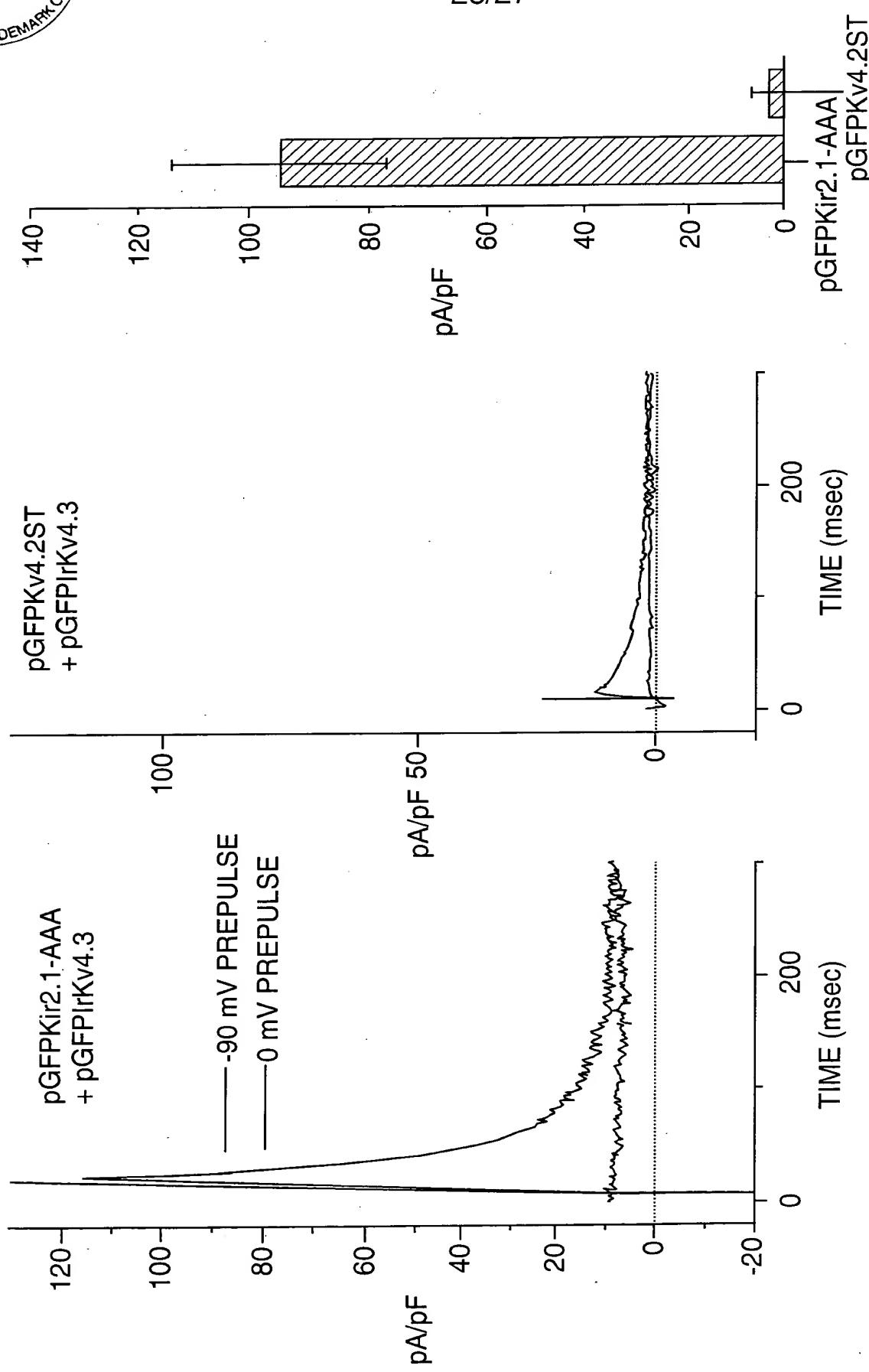


FIG. 14G

FIG. 14H

FIG. 14I



27/27



FIG. 15B



FIG. 15A

BEST AVAILABLE COPY